



SEQUENCE LISTING

<110> ARCANGEL, Phillip
CHIENT, David Y.

<120> HCV ASSAY

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<150> 60/409,515

<151> 2002-09-09

<160> 9

<170> PatentIn version 3.2

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<211> 2058

<212> DNA

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<223> NS3/41 conformational epitope DNA sequence

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tgc	ata	atc	acc	agc	cta	act	ggc	cg	gac	aaa	aac	caa	gtg	gag	gg	96
Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	
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gag	gtc	cag	att	gtg	tca	act	gct	gcc	caa	acc	ttc	ctg	gca	acg	tgc	144
Glu	Val	Gln	Ile	Val	Ser	Thr	Ala	Ala	Gln	Thr	Phe	Leu	Ala	Thr	Cys	
	35						40				45					

atc	aat	ggg	gtg	tgc	tgg	act	gtc	tac	cac	ggg	gcc	gga	acg	agg	acc	192
Ile	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Thr	Arg	Thr	
	50					55					60					

atc	gcg	tca	ccc	aag	gg	cct	gtc	atc	cag	atg	tat	acc	aat	gta	gac	240
Ile	Ala	Ser	Pro	Lys	Gly	Pro	Val	Ile	Gln	Met	Tyr	Thr	Asn	Val	Asp	
	65				70				75					80		

caa	gac	ctt	gtg	ggc	tgg	ccc	gct	ccg	caa	gg	agc	cga	tca	ttg	aca	288
Gln	Asp	Leu	Val	Gly	Trp	Pro	Ala	Pro	Gln	Gly	Ser	Arg	Ser	Leu	Thr	
			85					90					95			

ccc	tgc	act	tgc	ggc	tcc	tcg	gac	ctt	tac	ctg	gtc	acg	agg	cac	gcc	336
Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	
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gat	gtc	att	ccc	gtg	cgc	cgg	cgg	gg	gat	agc	agg	ggc	agc	ctg	ctg	384
Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	
			115				120					125				

tcg	ccc	cgg	ccc	att	tcc	tac	ttg	aaa	ggc	tcc	tcg	ggg	gg	ccg	ctg	432
Ser	Pro	Arg	Pro	Ile	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	
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acc cgt gga gtg gct aag gcg gtg gac ttt atc cct gtg gag aac cta	528
Thr Arg Gly Val Ala Lys Ala Val Asp Phe Ile Pro Val Glu Asn Leu	
165 170 175	
gag aca acc atg agg tcc ccg gtg ttc acg gat aac tcc tct cca cca	576
Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro	
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Val Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly	
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Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly	
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gtg aga aca att acc act ggc agc ccc atc acg tac tcc acc tac ggc	816
Val Arg Thr Ile Thr Thr Gly Ser Pro Ile Thr Tyr Ser Thr Tyr Gly	
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aag ttc ctt gcc gac ggc ggg tgc tgc ggg ggc gct tat gac ata ata	864
Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile	
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Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val	
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Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn	
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Ile Glu Glu Val Ala Leu Ser Thr Thr Gly Glu Ile Pro Phe Tyr Gly	
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Lys Ala Ile Pro Leu Glu Val Ile Lys Gly Gly Arg His Leu Ile Phe	
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Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Val Ala	
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gtc acc cag aca gtc gat ttc agc ctt gac cct acc ttc acc att gag Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu 435 440 445	1344
aca atc acg ctc ccc caa gat gct gtc tcc cgc act caa cgt cgg ggc Thr Ile Thr Leu Pro Gln Asp Ala Val Ser Arg Thr Gln Arg Arg Gly 450 455 460	1392
agg act ggc agg ggg aag cca ggc atc tac aga ttt gtg gca ccg ggg Arg Thr Gly Arg Gly Lys Pro Gly Ile Tyr Arg Phe Val Ala Pro Gly 465 470 475 480	1440
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gcc cac ttt cta tcc cag aca aag cag agt ggg gag aac ctt cct tac Ala His Phe Leu Ser Gln Thr Lys Gln Ser Gly Glu Asn Leu Pro Tyr 545 550 555 560	1680
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 Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Thr Gly Cys Val Val
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ata gtg ggc agg gtc gtc ttg tcc ggg aag ccg gca atc ata cct gac 2016
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 35 40 45
 Ile Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Thr Arg Thr
 50 55 60
 Ile Ala Ser Pro Lys Gly Pro Val Ile Gln Met Tyr Thr Asn Val Asp
 65 70 75 80
 Gln Asp Leu Val Gly Trp Pro Ala Pro Gln Gly Ser Arg Ser Leu Thr
 85 90 95
 Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala
 100 105 110
 Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu
 115 120 125
 Ser Pro Arg Pro Ile Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu
 130 135 140
 Leu Cys Pro Ala Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys
 145 150 155 160
 Thr Arg Gly Val Ala Lys Ala Val Asp Phe Ile Pro Val Glu Asn Leu
 165 170 175

Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro
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 Val Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly
 195 200 205
 Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr
 210 215 220
 Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly
 225 230 235 240
 Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly
 245 250 255
 Val Arg Thr Ile Thr Thr Gly Ser Pro Ile Thr Tyr Ser Thr Tyr Gly
 260 265 270
 Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile
 275 280 285
 Ile Cys Asp Glu Cys His Ser Thr Asp Ala Thr Ser Ile Leu Gly Ile
 290 295 300
 Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val
 305 310 315 320
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 325 330 335
 Ile Glu Glu Val Ala Leu Ser Thr Thr Gly Glu Ile Pro Phe Tyr Gly
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 355 360 365
 Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Val Ala
 370 375 380
 Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val
 385 390 395 400
 Ile Pro Pro Ile Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met
 405 410 415
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 420 425 430
 Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu
 435 440 445
 Thr Ile Thr Leu Pro Gln Asp Ala Val Ser Arg Thr Gln Arg Arg Gly
 450 455 460
 Arg Thr Gly Arg Gly Lys Pro Gly Ile Tyr Arg Phe Val Ala Pro Gly
 465 470 475 480
 Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr
 485 490 495

Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Thr Val
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 Arg Leu Arg Ala Tyr Met Asn Thr Pro Gly Leu Pro Val Cys Gln Asp
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 His Leu Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr His Ile Asp
 530 535 540
 Ala His Phe Leu Ser Gln Thr Lys Gln Ser Gly Glu Asn Leu Pro Tyr
 545 550 555 560
 Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro
 565 570 575
 Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr
 580 585 590
 Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn
 595 600 605
 Glu Ile Thr Leu Thr His Pro Val Thr Lys Tyr Ile Met Thr Cys Met
 610 615 620
 Ser Ala Asp Leu Glu Val Val Thr Ser Thr Trp Val Leu Val Gly Gly
 625 630 635 640
 Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Thr Gly Cys Val Val
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 Gly Ile Ile Asn Phe Glu Gln Lys Glu Ser Asn Gly Pro Val Lys Val
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 Trp Gly Ser Ile Lys Gly Leu Thr Glu Gly Leu His Gly Phe His Val
 35 40 45
 cat gag ttt gga gat aat aca gca ggc tgt acc agt gca ggt cct cac 192
 His Glu Phe Gly Asp Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His
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ttt aat cct cta tcc acg cgt ggt tgc aat tgc tct atc tat ccc ggc	240
Phe Asn Pro Leu Ser Thr Arg Gly Cys Asn Cys Ser Ile Tyr Pro Gly	
65 70 75 80	
cat ata acg ggt cac cgc atg gca tgg aag ctt ggt tcc gcc gcc aga	288
His Ile Thr Gly His Arg Met Ala Trp Lys Leu Gly Ser Ala Ala Arg	
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act acc tcg ggc ttt gtc tcc ttg ttc gcc cca ggt gcc aaa caa aac	336
Thr Thr Ser Gly Phe Val Ser Leu Phe Ala Pro Gly Ala Lys Gln Asn	
100 105 110	
gaa act cac gtc acg gga ggc gca gcc gcc cga act acg tct ggg ttg	384
Glu Thr His Val Thr Gly Gly Ala Ala Ala Arg Thr Thr Ser Gly Leu	
115 120 125	
acc tct ttg ttc tcc cca ggt gcc agc caa aac att caa ttg att act	432
Thr Ser Leu Phe Ser Pro Gly Ala Ser Gln Asn Ile Gln Leu Ile Thr	
130 135 140	
agt acg gat aac tcc tct cca cca gta gtg ccc cag agc ttc cag gtg	480
Ser Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val	
145 150 155 160	
gct cac ctc cat gct ccc aca ggc agc ggc aaa agc acc aag gtc ccg	528
Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro	
165 170 175	
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tcg ggg ggc gct tat gac ata ata att tgt gac gag tgc cac tcc acg	768
Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr	
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gat gcc aca tcc atc ttg ggc atc ggc act gtc ctt gac caa gca gag	816
Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu	
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Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly	
275 280 285	
tcc gtc act gtg ccc cat ccc aac atc gag gag gtt gct ctg tcc acc	912
Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr	
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 Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Lys Asp Arg Arg Ser
 805 810 815

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 50 55 60
 Phe Asn Pro Leu Ser Thr Arg Gly Cys Asn Cys Ser Ile Tyr Pro Gly
 65 70 75 80
 His Ile Thr Gly His Arg Met Ala Trp Lys Leu Gly Ser Ala Ala Arg
 85 90 95
 Thr Thr Ser Gly Phe Val Ser Leu Phe Ala Pro Gly Ala Lys Gln Asn
 100 105 110
 Glu Thr His Val Thr Gly Gly Ala Ala Ala Arg Thr Thr Ser Gly Leu
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 Thr Ser Leu Phe Ser Pro Gly Ala Ser Gln Asn Ile Gln Leu Ile Thr
 130 135 140
 Ser Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val
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 Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser
 180 185 190
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 195 200 205

Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser
 210 215 220
 Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys
 225 230 235 240
 Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr
 245 250 255
 Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu
 260 265 270
 Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly
 275 280 285
 Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr
 290 295 300
 Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile
 305 310 315 320
 Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp
 325 330 335
 Glu Leu Ala Ala Lys Leu Val Ala Leu Gly Ile Asn Ala Val Ala Tyr
 340 345 350
 Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val Val
 355 360 365
 Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp
 370 375 380
 Ser Val Ile Asp Cys Asn Thr Cys Ala Cys Ser Gly Lys Pro Ala Ile
 385 390 395 400
 Ile Pro Asp Arg Glu Val Leu Tyr Arg Glu Phe Asp Glu Met Glu Glu
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 Gln Phe Lys Gln Lys Ala Leu Gly Leu Ser Arg Gly Gly Lys Pro Ala
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 Ile Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu
 450 455 460
 Glu Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala
 465 470 475 480
 His Gln Phe Lys Glu Lys Val Leu Gly Leu Ile Asp Asn Asp Gln Val
 485 490 495
 Val Val Thr Pro Asp Lys Glu Ile Leu Tyr Glu Ala Phe Asp Glu Met
 500 505 510
 Glu Glu Cys Ala Ser Lys Ala Ala Leu Ile Glu Glu Gly Gln Arg Met
 515 520 525

Ala Glu Met Leu Lys Ser Lys Ile Gln Gly Leu Leu Gly Ile Leu Arg
 530 535 540
 Arg His Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu
 545 550 555 560
 Ile Ala Phe Ala Ser Arg Gly Asn His Val Ser Pro Thr His Tyr Val
 565 570 575
 Pro Ser Arg Ser Arg Arg Phe Ala Gln Ala Leu Pro Val Trp Ala Arg
 580 585 590
 Pro Asp Tyr Asn Pro Pro Leu Val Glu Thr Trp Lys Lys Pro Asp Tyr
 595 600 605
 Glu Pro Pro Val Val His Gly Arg Ser Ser Arg Arg Phe Ala Gln Ala
 610 615 620
 Leu Pro Val Trp Ala Arg Pro Asp Tyr Asn Pro Pro Leu Val Glu Thr
 625 630 635 640
 Trp Lys Lys Pro Asp Tyr Glu Pro Pro Val Val His Gly Arg Lys Thr
 645 650 655
 Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly
 660 665 670
 Gly Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg
 675 680 685
 Leu Gly Val Leu Ala Thr Arg Lys Thr Ser Pro Ile Pro Lys Ala Arg
 690 695 700
 Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro Leu
 705 710 715 720
 Tyr Gly Asn Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly Lys Pro
 725 730 735
 Gly Tyr Pro Trp Pro Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro
 740 745 750
 Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr
 755 760 765
 Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Leu Ala Thr Arg Lys
 770 775 780
 Thr Ser Pro Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala
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 Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Lys Asp Arg Arg Ser
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 Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro ;
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<211> 3297
 <212> DNA
 <213> Artificial

<220>
 <223> MEFA 7.1 DNA sequence

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Met Ala Thr Lys Ala Val Cys Val Leu Lys Gly Asp Gly Pro Val Gln
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ggt att att aac ttc gag cag aag gaa agt aat gga cca gtg aag gtg 96
Gly Ile Ile Asn Phe Glu Gln Lys Glu Ser Asn Gly Pro Val Lys Val
20 25 30

tgg gga agc att aaa gga ctg act gaa ggc ctg cat gga ttc cat gtt 144
Trp Gly Ser Ile Lys Gly Leu Thr Glu Gly Leu His Gly Phe His Val
35 40 45

cat gag ttt gga gat aat aca gca ggc tgt acc agt gca ggt cct cac 192
His Glu Phe Gly Asp Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His
50 55 60

ttt aat cct cta tcc aga aaa cac ggt ggg cca aag gat gaa gag agg 240
Phe Asn Pro Leu Ser Arg Lys His Gly Gly Pro Lys Asp Glu Glu Arg
65 70 75 80

cat gtt gga gac ttg ggc aat gtg act gct gac aaa gat ggt gtg gcc 288
His Val Gly Asp Leu Gly Asn Val Thr Ala Asp Lys Asp Gly Val Ala
85 90 95

gat gtg tct att gaa gat tct gtg atc tca ctc tca gga gac cat tgc 336
Asp Val Ser Ile Glu Asp Ser Val Ile Ser Leu Ser Gly Asp His Cys
100 105 110

atc att ggc cgc aca ctg gtg gtc cat gaa aaa gca gat gac ttg ggc 384
Ile Ile Gly Arg Thr Leu Val Val His Glu Lys Ala Asp Asp Leu Gly
115 120 125

aaa ggt gga aat gaa gaa agt aca aag aca gga aac gct gga agt cgt 432
Lys Gly Gly Asn Glu Glu Ser Thr Lys Thr Gly Asn Ala Gly Ser Arg
130 135 140

ttg gct tgt ggt gta att ggg atc gcc cag aat ttg aat tct ggt tgc 480
Leu Ala Cys Gly Val Ile Gly Ile Ala Gln Asn Leu Asn Ser Gly Cys
145 150 155 160

aat tgc tct atc tat ccc ggc cat ata acg ggt cac cgc atg gca tgg 528
Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp
165 170 175

aag ctt ggt tcc gcc gcc aga act acc tcg ggc ttt gtc tcc ttg ttc 576
Lys Leu Gly Ser Ala Ala Arg Thr Thr Ser Gly Phe Val Ser Leu Phe
180 185 190

gcc cca ggt gcc aaa caa aac gaa act cac gtc acg gga ggc gca gcc 624
Ala Pro Gly Ala Lys Gln Asn Glu Thr His Val Thr Gly Gly Ala Ala
195 200 205

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Ala Arg Thr Thr Ser Gly Leu Thr Ser Leu Phe Ser Pro Gly Ala Ser	
210 215 220	
caa aac att caa ttg att gtc gac ttt atc cct gtg gag aac cta gag	720
Gln Asn Ile Gln Leu Ile Val Asp Phe Ile Pro Val Glu Asn Leu Glu	
225 230 235 240	
aca acc atg cga tct ccg gtg ttc acg gat aac tcc tct cca cca gta	768
Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Val	
245 250 255	
gtg ccc cag agc ttc cag gtg gct cac ctc cat gct ccc aca ggc agc	816
Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser	
260 265 270	
ggc aaa agc acc aag gtc ccg gct gca tat gca gct cag ggc tat aag	864
Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys	
275 280 285	
gtg cta gta ctc aac ccc tct gtt gct gca aca ctg ggc ttt ggt gct	912
Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala	
290 295 300	
tac atg tcc aag gct cat ggg atc gat cct aac atc agg acc ggg gtg	960
Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val	
305 310 315 320	
aga aca att acc act ggc agc ccc atc acg tac tcc acc tac ggc aag	1008
Arg Thr Ile Thr Thr Gly Ser Pro Ile Thr Tyr Ser Thr Tyr Gly Lys	
325 330 335	
ttc ctt gcc gac ggc ggg tgc tgc ggg ggc gct tat gac ata ata att	1056
Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile	
340 345 350	
tgt gac gag tgc cac tcc acg gat gcc aca tcc atc ttg ggc att ggc	1104
Cys Asp Glu Cys His Ser Thr Asp Ala Thr Ser Ile Leu Gly Ile Gly	
355 360 365	
act gtc ctt gac caa gca gag act gcg ggg gcg aga ctg gtt gtg ctc	1152
Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu	
370 375 380	
gcc acc gcc acc cct ccg ggc tcc gtc act gtg ccc cat ccc aac atc	1200
Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile	
385 390 395 400	
gag gag gtt gct ctg tcc acc acc gga gag atc cct ttt tac ggc aag	1248
Glu Glu Val Ala Leu Ser Thr Thr Gly Glu Ile Pro Phe Tyr Gly Lys	
405 410 415	
gct atc ccc ctc gaa gta atc aag ggg ggg aga cat ctc atc ttc tgt	1296
Ala Ile Pro Leu Glu Val Ile Lys Gly Gly Arg His Leu Ile Phe Cys	
420 425 430	
cat tca aag aag aag tgc gac gaa ctc gcc gca aag ctg gtc gca ttg	1344
His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Val Ala Leu	
435 440 445	

ggc atc aat gcc gtg gcc tac tac cgc ggt ctt gac gtg tcc gtc atc Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile 450 455 460	1392
ccg acc agc ggc gat gtt gtc gtc gtg gca acc gat gcc ctc atg acc Pro Thr Ser Gly Asp Val Val Val Ala Thr Asp Ala Leu Met Thr 465 470 475 480	1440
ggc tat acc ggc gac ttc gac tcg gtg ata gac tgc aat acg tgt gtc Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val 485 490 495	1488
acc cag aca gtc gat ttc agc ctt gac cct acc ttc acc att gag aca Thr Gln Thr Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr 500 505 510	1536
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act ggc agg ggg aag cca ggc atc tac aga ttt gtg gca ccg ggg gag Thr Gly Arg Gly Lys Pro Gly Ile Tyr Arg Phe Val Ala Pro Gly Glu 530 535 540	1632
cgc ccc tcc ggc atg ttc gac tcg tcc gtc ctc tgt gag tgc tat gac Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp 545 550 555 560	1680
gca ggc tgt gct tgg tat gag ctc acg ccc gcc gag act aca gtt agg Ala Gly Cys Ala Thr Trp Tyr Glu Leu Thr Pro Ala Glu Thr Thr Val Arg 565 570 575	1728
cta cga gcg tac atg aac acc ccg ggg ctt ccc gtg tgc cag gac cat Leu Arg Ala Tyr Met Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His 580 585 590	1776
ctt gaa ttt tgg gag ggc gtc ttt aca ggc ctc act cat ata gat gcc Leu Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr His Ile Asp Ala 595 600 605	1824
cac ttt cta tcc cag aca aag cag agt ggg gag aac ctt cct tac ctg His Phe Leu Ser Gln Thr Lys Gln Ser Gly Glu Asn Leu Pro Tyr Leu 610 615 620	1872
gta gcg tac caa gcc acc gtg tgc gct agg gct caa gcc cct ccc cca Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro 625 630 635 640	1920
tcg tgg gac cag atg tgg aag tgt ttg att cgc ctc aag ccc acc ctc Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu 645 650 655	1968
cat ggg cca aca ccc ctg cta tac aga ctg ggc gct gtt cag aat gaa His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu 660 665 670	2016
atc acc ctg acg cac cca gtc acc aaa tac atc atg aca tgc atg tcg Ile Thr Leu Thr His Pro Val Thr Lys Tyr Ile Met Thr Cys Met Ser 675 680 685	2064

gcc gac ctg gag gtc gtc acg agc gca tgc tcc ggg aag cag gca atc Ala Asp Leu Glu Val Val Thr Ser Ala Cys Ser Gly Lys Pro Ala Ile 690 695 700	2112
ata cct gac agg gaa gtc ctc tac cga gag ttc gat gag atg gaa gag Ile Pro Asp Arg Glu Val Leu Tyr Arg Glu Phe Asp Glu Met Glu Glu 705 710 715 720	2160
tgc tct cag cac tta cag tac atc gag caa ggg atg atg ctc gcc gag Cys Ser Gln His Leu Pro Tyr Ile Glu Gln Gly Met Met Leu Ala Glu 725 730 735	2208
cag ttc aag cag aag gcc ctc ggc ctc tgc cga ggg ggc aag cag gca Gln Phe Lys Glu Lys Ala Leu Gly Leu Ser Arg Gly Lys Lys Pro Ala 740 745 750	2256
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gag tgc tca caa gct gcc cca tat atc gaa caa gct cag gta ata gct Glu Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala 770 775 780	2352
cac cag ttc aag gaa aaa gtc ctt gga ttg atc gat aat gat caa gtg His Gln Phe Lys Glu Lys Val Leu Gly Leu Ile Asp Asn Asp Gln Val 785 790 795 800	2400
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gaa gaa tgc gcc tcc aaa gcc gcc ctc att gag gaa ggg cag cgg atg Glu Glu Cys Ala Ser Lys Ala Ala Leu Ile Glu Glu Gly Gln Arg Met 820 825 830	2496
gcg gag atg ctc aag tct aag ata caa ggc ctc ctc ggg ata ctg cgc Ala Glu Met Leu Lys Ser Lys Ile Gln Gly Leu Leu Gly Ile Leu Arg 835 840 845	2544
cgg cac gtt ggt cct ggc gag ggg gca gtg cag tgg atg aac cgg ctg Arg His Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu 850 855 860	2592
ata gcc ttc gcc tcc aga ggg aac cat gtt tcc ccc acg cac tac gtt Ile Ala Phe Ala Ser Arg Gly Asn His Val Ser Pro Thr His Tyr Val 865 870 875 880	2640
ccg tct aga tcc cgg aga ttc gcc cag gcc ctg ccc gtt tgg cgc cgg Pro Ser Arg Ser Arg Arg Phe Ala Gln Ala Leu Pro Val Trp Ala Arg 885 890 895	2688
ccg gac tat aac ccc cag cta gtg gag acg tgg aaa aag ccc gac tac Pro Asp Tyr Asn Pro Pro Leu Val Glu Thr Trp Lys Lys Pro Asp Tyr 900 905 910	2736
gaa cca cct gtg gtc cac ggc aga tct tct cgg aga ttc gcc cag gcc Glu Pro Pro Val Val His Gly Arg Ser Ser Arg Arg Phe Ala Gln Ala 915 920 925	2784

ctg ccc gtt tgg gcg cgg ccg gac tat aac ccc ccg cta gtg gag acg 2832
 Leu Pro Val Trp Ala Arg Pro Asp Tyr Asn Pro Pro Leu Val Glu Thr
 930 935 940

tgg aaa aag ccc gac tac gaa cca cct gtg gtc cat ggc aga aag acc 2880
 Trp Lys Lys Pro Asp Tyr Glu Pro Pro Val Val His Gly Arg Lys Thr
 945 950 955 960

aaa cgt aac acc aac cgg cgg ccg cag gac gtc aag ttc ccg ggt ggc 2928
 Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly
 965 970 975

ggt cag atc gtt ggt cgc agg ggc cct cct atc ccc aag gct cgt cgg 2976
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 980 985 990

ccc gag ggc agg acc tgg gct cag ccc ggt tac cct tgg ccc ctc tat 3024
 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr
 995 1000 1005

ggc aat aag gac aga cgg tct aca ggt aag tcc tgg ggt aag cca ggg 3072
 Gly Asn Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly
 1010 1015 1020

tac cct tgg cca aga aag acc aaa cgt aac acc aac cga cgg ccg cag 3120
 Tyr Pro Trp Pro Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln
 1025 1030 1035 1040

gac gtc aag ttc ccg ggt ggc ggt cag atc gtt ggt cgc agg ggc cct 3168
 Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Arg Arg Gly Pro
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cct atc ccc aag gct cgt cgg ccc gag ggc agg acc tgg gct cag ccc 3216
 Pro Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro
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ggt tac cct tgg ccc ctc tat ggc aat aag gac aga cgg tct acc ggt 3264
 Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Lys Asp Arg Arg Ser Thr Gly
 1075 1080 1085

aag tcc tgg ggt aag cca ggg tat cct tgg ccc 3297
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 <213> Artificial

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 35 40 45
 His Glu Phe Gly Asp Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His
 50 55 60
 Phe Asn Pro Leu Ser Arg Lys His Gly Gly Pro Lys Asp Glu Glu Arg
 65 70 75 80
 His Val Gly Asp Leu Gly Asn Val Thr Ala Asp Lys Asp Gly Val Ala
 85 90 95
 Asp Val Ser Ile Glu Asp Ser Val Ile Ser Leu Ser Gly Asp His Cys
 100 105 110
 Ile Ile Gly Arg Thr Leu Val Val His Glu Lys Ala Asp Asp Leu Gly
 115 120 125
 Lys Gly Gly Asn Glu Glu Ser Thr Lys Thr Gly Asn Ala Gly Ser Arg
 130 135 140
 Leu Ala Cys Gly Val Ile Gly Ile Ala Gln Asn Leu Asn Ser Gly Cys
 145 150 155 160
 Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp
 165 170 175
 Lys Leu Gly Ser Ala Ala Arg Thr Thr Ser Gly Phe Val Ser Leu Phe
 180 185 190
 Ala Pro Gly Ala Lys Gln Asn Glu Thr His Val Thr Gly Gly Ala Ala
 195 200 205
 Ala Arg Thr Thr Ser Gly Leu Thr Ser Leu Phe Ser Pro Gly Ala Ser
 210 215 220
 Gln Asn Ile Gln Leu Ile Val Asp Phe Ile Pro Val Glu Asn Leu Glu
 225 230 235 240
 Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Val
 245 250 255
 Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser
 260 265 270
 Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys
 275 280 285
 Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala
 290 295 300

Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val
 305 310 315 320
 Arg Thr Ile Thr Thr Gly Ser Pro Ile Thr Tyr Ser Thr Tyr Gly Lys
 325 330 335
 Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile
 340 345 350
 Cys Asp Glu Cys His Ser Thr Asp Ala Thr Ser Ile Leu Gly Ile Gly
 355 360 365
 Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu
 370 375 380
 Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile
 385 390 395 400
 Glu Glu Val Ala Leu Ser Thr Thr Gly Glu Ile Pro Phe Tyr Gly Lys
 405 410 415
 Ala Ile Pro Leu Glu Val Ile Lys Gly Gly Arg His Leu Ile Phe Cys
 420 425 430
 His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Val Ala Leu
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 Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile
 450 455 460
 Pro Thr Ser Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met Thr
 465 470 475 480
 Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val
 485 490 495
 Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr
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 Ile Thr Leu Pro Gln Asp Ala Val Ser Arg Thr Gln Arg Arg Gly Arg
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 Thr Gly Arg Gly Lys Pro Gly Ile Tyr Arg Phe Val Ala Pro Gly Glu
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 Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp
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 Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Thr Val Arg
 565 570 575
 Leu Arg Ala Tyr Met Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His
 580 585 590
 Leu Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr His Ile Asp Ala
 595 600 605

His Phe Leu Ser Gln Thr Lys Gln Ser Gly Glu Asn Leu Pro Tyr Leu
 610 615 620
 Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro
 625 630 635 640
 Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu
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 His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu
 660 665 670
 Ile Thr Leu Thr His Pro Val Thr Lys Tyr Ile Met Thr Cys Met Ser
 675 680 685
 Ala Asp Leu Glu Val Val Thr Ser Ala Cys Ser Gly Lys Pro Ala Ile
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 Ile Pro Asp Arg Glu Val Leu Tyr Arg Glu Phe Asp Glu Met Glu Glu
 705 710 715 720
 Cys Ser Gln His Leu Pro Tyr Ile Glu Gln Gly Met Met Leu Ala Glu
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 Gln Phe Lys Gln Lys Ala Leu Gly Leu Ser Arg Gly Gly Lys Pro Ala
 740 745 750
 Ile Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu
 755 760 765
 Glu Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala
 770 775 780
 His Gln Phe Lys Glu Lys Val Leu Gly Leu Ile Asp Asn Asp Gln Val
 785 790 795 800
 Val Val Thr Pro Asp Lys Glu Ile Leu Tyr Glu Ala Phe Asp Glu Met
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 Glu Glu Cys Ala Ser Lys Ala Ala Leu Ile Glu Glu Gly Gln Arg Met
 820 825 830
 Ala Glu Met Leu Lys Ser Lys Ile Gln Gly Leu Leu Gly Ile Leu Arg
 835 840 845
 Arg His Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu
 850 855 860
 Ile Ala Phe Ala Ser Arg Gly Asn His Val Ser Pro Thr His Tyr Val
 865 870 875 880
 Pro Ser Arg Ser Arg Arg Phe Ala Gln Ala Leu Pro Val Trp Ala Arg
 885 890 895
 Pro Asp Tyr Asn Pro Pro Leu Val Glu Thr Trp Lys Lys Pro Asp Tyr
 900 905 910

Glu Pro Pro Val Val His Gly Arg Ser Ser Arg Arg Phe Ala Gln Ala
915 920 925

Leu Pro Val Trp Ala Arg Pro Asp Tyr Asn Pro Pro Leu Val Glu Thr
930 935 940

Trp Lys Lys Pro Asp Tyr Glu Pro Pro Val Val His Gly Arg Lys Thr
945 950 955 960

Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly
965 970 975

Gly Gln Ile Val Gly Arg Arg Gly Pro Pro Ile Pro Lys Ala Arg Arg
980 985 990

Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr
995 1000 1005

Gly Asn Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly
1010 1015 1020

Tyr Pro Trp Pro Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln
1025 1030 1035 1040

Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Arg Arg Gly Pro
1045 1050 1055

Pro Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro
1060 1065 1070

Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Lys Asp Arg Arg Ser Thr Gly
1075 1080 1085

Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
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Gly Ala Lys Gln Asn
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<220>

<223> sequence following HindIII site

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acaaaacaaa

10

<210> 9

<211> 23

<212> PRT

<213> Artificial

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<223> NS4A peptide

<400> 9

Lys Lys Gly Ser Val Val Ile Val Gly Arg Ile Val Leu Ser Gly Lys
1 5 10 15

Pro Ala Ile Ile Pro Lys Lys
20